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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/597,796CDATE: 03/20/2003
TIME: 16:10:20Input Set : A:\-90-5.app
Output Set: N:\CRF4\03202003\I597796C.raw

3 <110> APPLICANT: Skeiky, Yasir
 4 Reed, Steven
 5 Alderson, Mark
 6 Corixa Corporation
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 10 <130> FILE REFERENCE: 014058-009050US
 12 <140> CURRENT APPLICATION NUMBER: US 09/597,796C
 13 <141> CURRENT FILING DATE: 2000-06-20
 15 <150> PRIOR APPLICATION NUMBER: US 09/056,556
 16 <151> PRIOR FILING DATE: 1998-04-07
 18 <150> PRIOR APPLICATION NUMBER: US 09/223,040
 19 <151> PRIOR FILING DATE: 1998-12-30
 21 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/07717
 22 <151> PRIOR FILING DATE: 1999-04-07
 24 <150> PRIOR APPLICATION NUMBER: US 09/287,849
 25 <151> PRIOR FILING DATE: 1999-04-07
 27 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 28 <151> PRIOR FILING DATE: 1999-10-07
 30 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 31 <151> PRIOR FILING DATE: 1999-10-07
 33 <160> NUMBER OF SEQ ID NOS: 30
 35 <170> SOFTWARE: PatentIn Ver. 2.1
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 588
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Mycobacterium tuberculosis
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)..(588)
 48 <223> OTHER INFORMATION: Ra35
 50 <400> SEQUENCE: 1
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 52 tccgcgatgg tcgcccaga gtggccacag gtggtaaca tcaacaccaa actgggtac 120
 53 aacaacgccc tgggcggccgg gaccggcatc gtcatcgatc ccaacgggtgt cgtgctgacc 180
 54 aacaaccacg tgatcgccgg cgccaccgac atcaatgcgt tcagcgtcgg ctccggccaa 240
 55 acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgcggt gctgcagctg 300
 56 cgggtgccg gtggcctacc atcggccggc atcgggtggc gcgtcgcggt tggtagcccc 360
 57 gtcgtcgca tgggcaacag cgggtggcag ggcggaaacgc cccgtcgggt gcctggcagg 420
 58 gtggtcgcgc tcggccaaac cgtgcaggcg tcggattcgc tgaccggtgc cgaagagaca 480
 59 ttgaacgggt tgatccagtt cgtatcgccg atccagcccc gtgattcggg cgggccccgtc 540
 60 gtcaacggcc taggacaggt ggtcggtatg aacacggccg cgtcctag 588

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Input Set : A:\-90-5.app

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63 <210> SEQ ID NO: 2
 64 <211> LENGTH: 195
 65 <212> TYPE: PRT
 66 <213> ORGANISM: *Mycobacterium tuberculosis*
 68 <220> FEATURE:
 69 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)
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 73 1 5 10 15
 74 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 75 20 25 30
 76 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 77 35 40 45
 78 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 79 50 55 60
 80 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 81 65 70 75 80
 82 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 83 85 90 95
 84 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 85 100 105 110
 86 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 87 115 120 125
 88 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 89 130 135 140
 90 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 91 145 150 155 160
 92 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 93 165 170 175
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 95 180 185 190
 96 Ala Ala Ser
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 101 <211> LENGTH: 1872
 102 <212> TYPE: DNA
 103 <213> ORGANISM: *Mycobacterium tuberculosis*
 105 <220> FEATURE:
 106 <223> OTHER INFORMATION: MTB32A (TbRa35FL) cDNA
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 109 <221> NAME/KEY: modified_base
 110 <222> LOCATION: (1460)
 111 <223> OTHER INFORMATION: n = g, a, c or t
 113 <220> FEATURE:
 114 <221> NAME/KEY: modified_base
 115 <222> LOCATION: (1854)
 116 <223> OTHER INFORMATION: n = g, a, c or t
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120 tagctacccc gacacaggag gttacggat gagcaattcg cgccgcccgt cactcaggtg 120
 121 gtcatggttg ctgagcgtgc tggctccgt cgggctggc ctggccacgg cgccggccca 180
 122 ggcggccccc cccgccttgt cgcaaggaccg gttcggccac ttcccccgcg tgcccctcga 240
 123 cccgtcccgat atggtcgccc aagtggcgc acagggtgtc aacatcaaca ccaaactggg 300
 124 ctacaacaac gccgtggcg cccggaccgg catcgatcatc gatcccaacg gtgtcgtgct 360
 125 gaccaacaac cacgtgatcg cgggcgcac cgcacatcaat gcgttcagcg tcggctccgg 420
 126 ccaaaccatac ggcgtcgatg tggcgggtg tgaccgcacc caggatgtcg cgggtcgca 480
 127 gctgcgcgg gccgggtggc tgccgtcggt ggcgatcggt ggcggcggtcg cgggtggta 540
 128 gcccgtcgatc gcatgggca acagcggtgg gcaggcgga acgccccgtg cgggtcctgg 600
 129 cagggtggtc ggcgtcggcc aaaccgtgca ggcgtcgatg tcgctgaccg gtgcccgaaga 660
 130 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccgggtgatt cgggggggccc 720
 131 cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
 132 gctgtcccag ggtgggcagg gattcgccat tccgatcggt caggcgatgg cgatcgcggg 840
 133 ccaaatccga tcgggtgggg ggtcacccac cgttcatatc gggcctaccg ctttcctcg 900
 134 ctgggtgtt gtcgacaaca acggcaacgg cgacacgatc caacgcgtgg tcggaagcgc 960
 135 tccggcggca agtctcgca ttcaccggc cgacgtgatc accgcgggtcg acggcgctcc 1020
 136 gatcaactcg gccaccgcg tggcggacgc gcttaacggg catcatcccg gtgacgtcat 1080
 137 ctcggtaac tggcaaaacca agtcggcggt caccgtatac gggacgtga cattggccga 1140
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 139 cagccgtgat tggcgcgtga gcccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
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 142 gatccgaccc ggttaagca cggcgtcttc tacgggtgc tggccggc gttcttcgac 1440
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 144 tggcttggca tcgactgcat ctgttgcgc ctgcgttacg actcaccgt gcgcgacggc 1560
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 146 gtcgcctgg tcgacaccgc tcaccggcga ggtatccgca tcatcaccga cctgggtatg 1680
 147 aatcacaccc cggagtcgca cccctggttt caggatccc gccgcgaccc agacggaccg 1740
 148 tacggtgact attacgtgtg gagcgcacacc agcgcgcgt acaccgcgc cggatcatc 1800
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 150 gcaccgattc tt 1872
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 155 <212> TYPE: PRT
 156 <213> ORGANISM: *Mycobacterium tuberculosis*
 158 <220> FEATURE:
 159 <223> OTHER INFORMATION: MTB32A (TbRa35FL) protein
 161 <400> SEQUENCE: 4
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 164 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 165 20 25 30
 166 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 167 35 40 45
 168 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 169 50 55 60
 170 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 171 65 70 75 80
 172 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val

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173 85 90 95
 174 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 175 100 105 110
 176 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 177 115 120 125
 178 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 179 130 135 140
 180 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 181 145 150 155 160
 182 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 183 165 170 175
 184 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 185 180 185 190
 186 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 187 195 200 205
 188 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 189 210 215 220
 190 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 191 225 230 235 240
 192 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 193 245 250 255
 194 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 195 260 265 270
 196 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 197 275 280 285
 198 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 199 290 295 300
 200 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 201 305 310 315 320
 202 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 203 325 330 335
 204 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
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 212 <212> TYPE: DNA
 213 <213> ORGANISM: Mycobacterium tuberculosis
 215 <220> FEATURE:
 216 <223> OTHER INFORMATION: MTBRA12 C-terminus of MTB32A (Ra35FL)
 218 <400> SEQUENCE: 5
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 220 cattccgatc gggcaggcga tggcgatcgc gggccagatc cgatcgggt gggggtcacc 120
 221 caccgttcat atcgggccta ccgccttcct cggctgggt gttgtcgaca acaacggcaa 180
 222 cggcgacacga gtccaaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
 223 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccc cgatggcgaa 300
 224 cgcgcctaac gggcatcata cccgtgacgt catctcggt aactggcaaa ccaagtgcgg 360
 225 cggcgcacgcgt acagggaacg tgacattggc cgagggaccc ccggcctgat ttcgtcgygg 420

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Input Set : A:\-90-5.app
Output Set: N:\CRF4\03202003\I597796C.raw

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 230 <211> LENGTH: 132
 231 <212> TYPE: PRT
 232 <213> ORGANISM: Mycobacterium tuberculosis
 234 <220> FEATURE:
 235 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)
 237 <400> SEQUENCE: 6
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 240 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 241 20 25 30
 242 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 243 35 40 45
 244 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 245 50 55 60
 246 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 247 65 70 75 80
 248 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 249 85 90 95
 250 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
 251 100 105 110
 252 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 253 115 120 125
 254 Gly Pro Pro Ala
 255 130
 258 <210> SEQ ID NO: 7
 259 <211> LENGTH: 3058
 260 <212> TYPE: DNA
 261 <213> ORGANISM: Mycobacterium tuberculosis
 263 <220> FEATURE:
 264 <223> OTHER INFORMATION: MTB39 (TbH9) cDNA full-length
 266 <400> SEQUENCE: 7
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 268 ggcataccca gagatgttgg cggcgccggc tgacaccctg cagagcatcg gtgttaccac 120
 269 tggcttagc aatgccctg cggcgcccc gacgactggg gtggccccc ccgtgcccga 180
 270 tgggtgtcg gcgctgactg cggcgactt cgccgcacat gccgcgtatgt atcagtccgt 240
 271 gagcgctcggt gctgctgcga ttcatgacca gttcgccggcc acccttgcac gcagcgccag 300
 272 ctcgtatgcg gccactgaag tcgcaatgc ggcggccggcc agctaagccaa ggaacagtcg 360
 273 gcacgagaaa ccacgagaaa tagggacacg taatggatgaa ttccggggcg ttaccaccgg 420
 274 agatcaactc cgcgaggatg tacgcccccc cgggttcggc ctcgctgggt gccgcggctc 480
 275 agatgtggga cagcggtggcg agtgcacgtt tttcgccgcgtt cagtcgggtgg 540
 276 tctggggctc gacgggtgggg tcgtggatag gttcgccgc gggctgtatg gtggccggcgg 600
 277 cctcgccgtt tggcggtgg atgagcgtca ccgcggggca ggccgagctg accgcccggcc 660
 278 aggtccgggt tgctcgccgc gcctacgaga cggcgatgg gctgacgggtg ccccccggcc 720
 279 tggatcgccga gaaccgtgtc gaactgtatgt ttctgtatgc gaccaacctc ttggggcaaa 780
 280 acaccccgcc gatcgccgtc aacgaggccc aatacggcga gatgtggggcc caagacgccc 840
 281 ccgcgtatgtt tggctacgccc gcggcgacgg cgacggcgac ggcacgttg ctggccgttcg 900
 282 aggaggcgcc ggagatgacc agcgccgggtg ggctccgtca gcaggccgccc gcgggtcgagg 960

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/597,796C

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Input Set : A:\-90-5.app
Output Set: N:\CRF4\03202003\I597796C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1460,1854
Seq#:11; N Pos. 30,33,2270
Seq#:17; N Pos. 497,500,1136,1445,1487,1509,1515
Seq#:25; N Pos. 767
Seq#:26; Xaa Pos. 254

VERIFICATION SUMMARY

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Input Set : A:\-90-5.app

Output Set: N:\CRF4\03202003\I597796C.raw

L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1440
M:341 Repeated in SeqNo=3
L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:480
M:341 Repeated in SeqNo=17
L:1100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:720
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:240
L:1204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27